SEQUENCE LISTING

<110> Lin, Biaoyang

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Nucleic Acids

<130> P-IS 4373

<140> US 09/821,812
<141> 2001-03-28

<160> 11

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gtt cag atc atc atc atc gtg gtg gtg atg atg gtg atg gtg gtg gtg    161
Val Gln Ile Ile Ile Ile Val Val Val Met Met Val Met Val Val Val
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atc acg tgc ctg ctg agc cac tac aag ctg tct gca cgg tcc ttc atc    209
Ile Thr Cys Leu Leu Ser His Tyr Lys Leu Ser Ala Arg Ser Phe Ile
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agc cgg cac agc cag ggg cgg agg aga gaa gat gcc ctg tcc tca gaa    257
Ser Arg His Ser Gln Gly Arg Arg Arg Glu Asp Ala Leu Ser Ser Glu
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gga tgc ctg tgg ccc tcg gag agc aca gtg tca ggc aac gga atc cca    305
Gly Cys Leu Trp Pro Ser Glu Ser Thr Val Ser Gly Asn Gly Ile Pro
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gag ccg cag gtc tac gcc ccg cct cgg ccc acc gac cgc ctg gcc gtg    353
Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro Thr Asp Arg Leu Ala Val
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ccg ccc ttc gcc cag cgg gag cgc ttc cac cgc ttc cag ccc acc tat    401
Pro Pro Phe Ala Gln Arg Glu Arg Phe His Arg Phe Gln Pro Thr Tyr
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ccg tac ctg cag cac gag atc gac ctg cca ccc acc atc tcg ctg tca    449
Pro Tyr Leu Gln His Glu Ile Asp Leu Pro Pro Thr Ile Ser Leu Ser
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Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly Pro Cys Thr Leu Gln Leu
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cgg gac ccc gag cag cag ctg gaa ctg aac cgg gag tcg gtg cgc gca    545
Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn Arg Glu Ser Val Arg Ala
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ccc cca aac aga acc atc ttc gac agt gac ctg atg gat agt gcc agg    593
Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp Leu Met Asp Ser Ala Arg
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ctg ggc ggc ccc tgc ccc ccc agc agt aac tcg ggc atc agc gcc acg    641
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tgc tac ggc agc ggc ggg cgc atg gag ggg ccg ccg ccc acc tac agc    689
Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly Pro Pro Pro Thr Tyr Ser
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Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr Arg Leu His His Thr His
215                 220                 225                 230

atc gcg ccc cta gag agc gca gcc atc tgg agc aaa gag aag gat aaa   833
Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp Ser Lys Glu Lys Asp Lys
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Gln Lys Gly His Pro Leu
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Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg Arg Glu
        35                  40                  45
Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr Val
    50                  55                  60
Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg Pro
65                  70                  75                  80
Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe His
                85                  90                  95
Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu Pro
            100                 105                 110
Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly
        115                 120                 125
Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn
    130                 135                 140
Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp
145                 150                 155                 160
Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser Asn
                165                 170                 175
Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu Gly
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            180                 185                 190
Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser Ser
        195                 200                 205
Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly Thr
    210                 215                 220
Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile Trp
225                 230                 235                 240
Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
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<223> Xaa=any amino acid

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ccg agg ctc tcc tgg agc gct ggg cct tcg ctg gcc gca ccg gca gcc   96
Pro Arg Leu Ser Trp Ser Ala Gly Pro Ser Leu Ala Ala Pro Ala Ala
             20                  25                  30

atg agc tcg gag atg gag ccg ctg ctc ctg gcc tgg agc tat ttt agg   144
Met Ser Ser Glu Met Glu Pro Leu Leu Leu Ala Trp Ser Tyr Phe Arg
         35                  40                  45

cgc agg aag ttc cag ctc tgc gcc gat cta tgc acg cag atg ctg gag   192
Arg Arg Lys Phe Gln Leu Cys Ala Asp Leu Cys Thr Gln Met Leu Glu
     50                  55                  60

aag tcc cct tat gac cag gca gct tgg atc tta aaa gca aga gcg cta   240
Lys Ser Pro Tyr Asp Gln Ala Ala Trp Ile Leu Lys Ala Arg Ala Leu
 65                  70                  75                  80

aca gaa atg gta tac ata gat gaa att gat gta gat cag gaa gga att   288
Thr Glu Met Val Tyr Ile Asp Glu Ile Asp Val Asp Gln Glu Gly Ile
                 85                  90                  95

gca gaa atg atg ctg gat gaa aat gct ata gct caa gtt cca cgc cct   336
Ala Glu Met Met Leu Asp Glu Asn Ala Ile Ala Gln Val Pro Arg Pro
            100                 105                 110
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gga acg tct ttg aaa ctc cct gga act aat cag aca gga ggg cct agc   384
Gly Thr Ser Leu Lys Leu Pro Gly Thr Asn Gln Thr Gly Gly Pro Ser
        115                 120                 125

cag gcc gtt agg cca atc aca caa gct gga aga ccc att aca ggt ttc   432
Gln Ala Val Arg Pro Ile Thr Gln Ala Gly Arg Pro Ile Thr Gly Phe
    130                 135                 140

ctc agg ccc agc acg cag agt gga agg cca ggc act atg gaa cag gct   480
Leu Arg Pro Ser Thr Gln Ser Gly Arg Pro Gly Thr Met Glu Gln Ala
145                 150                 155                 160

atc aga aca ccc aga acc gcc tac aca gcc cgc cct atc acc agc tcc   528
Ile Arg Thr Pro Arg Thr Ala Tyr Thr Ala Arg Pro Ile Thr Ser Ser
                165                 170                 175

tcc gga aga ttt gtc agg ctg gga acg gct tcc atg ctt aca agt cct   576
Ser Gly Arg Phe Val Arg Leu Gly Thr Ala Ser Met Leu Thr Ser Pro
            180                 185                 190

gat gga cca ttt ata aat tta tct agg ctg aat tta aca aag tat tcc   624
Asp Gly Pro Phe Ile Asn Leu Ser Arg Leu Asn Leu Thr Lys Tyr Ser
        195                 200                 205

cag aaa cct aag ttg gca aag gct tgt ttg agt ata tct ttc atc atg   672
Gln Lys Pro Lys Leu Ala Lys Ala Cys Leu Ser Ile Ser Phe Ile Met
    210                 215                 220

aaa atg atg tta aga ctg ctt tgg atc tgg ctg gcc ctc tcc aca gaa   720
Lys Met Met Leu Arg Leu Leu Trp Ile Trp Leu Ala Leu Ser Thr Glu
225                 230                 235                 240

cat tct cag tac aag gac tgg tgg tgg aaa gta cag att gga aaa tgt   768
His Ser Gln Tyr Lys Asp Trp Trp Trp Lys Val Gln Ile Gly Lys Cys
                245                 250                 255

tac tac agg ttg gga atg tat cgt gaa gca gaa aaa cag ttt aaa tca   816
Tyr Tyr Arg Leu Gly Met Tyr Arg Glu Ala Glu Lys Gln Phe Lys Ser
            260                 265                 270

gcc ctg aag cag cag gaa atg gta gat aca ttt ctg tac ttg gca aaa   864
Ala Leu Lys Gln Gln Glu Met Val Asp Thr Phe Leu Tyr Leu Ala Lys
        275                 280                 285

gtt tat gtc tca ttg gat caa cct gtg act gct tta aat ctt ttc aaa   912
Val Tyr Val Ser Leu Asp Gln Pro Val Thr Ala Leu Asn Leu Phe Lys
    290                 295                 300

caa ggc tta gat aag ttt cca gga gaa gta acc ctg ctc tgt gga att   960
Gln Gly Leu Asp Lys Phe Pro Gly Glu Val Thr Leu Leu Cys Gly Ile
305                 310                 315                 320

gca aga atc tat gag gaa atg aac aat atg tca tca gca gca gaa tat   1008
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Ala Arg Ile Tyr Glu Glu Met Asn Asn Met Ser Ser Ala Ala Glu Tyr
                325                 330                 335

tac aaa gaa gtt ttg aaa caa gac aat act cat gtg gra gcc atc gca   1056
Tyr Lys Glu Val Leu Lys Gln Asp Asn Thr His Val Xaa Ala Ile Ala
            340                 345                 350

tgc att gga agc aac cac ttc tat tct gat cag cca gaa ata gct ctc   1104
Cys Ile Gly Ser Asn His Phe Tyr Ser Asp Gln Pro Glu Ile Ala Leu
        355                 360                 365

cgg ttt tac agg cgg ctg ctg cag atg ggc att tat aac ggc cag ctt   1152
Arg Phe Tyr Arg Arg Leu Leu Gln Met Gly Ile Tyr Asn Gly Gln Leu
    370                 375                 380

ttt aac aat ctg ggg ctg tgt tgc ttc tat gcc cag cag tat gat atg   1200
Phe Asn Asn Leu Gly Leu Cys Cys Phe Tyr Ala Gln Gln Tyr Asp Met
385                 390                 395                 400

act ctg acc tca ttt gaa cgt gcc ctt tct ttg gct gaa aat gaa gaa   1248
Thr Leu Thr Ser Phe Glu Arg Ala Leu Ser Leu Ala Glu Asn Glu Glu
                405                 410                 415

gag gca gct gat gtc tgg tac aac ttg gga cat gta gct gtg gga ata   1296
Glu Ala Ala Asp Val Trp Tyr Asn Leu Gly His Val Ala Val Gly Ile
            420                 425                 430

gga gat aca aat ttg gcc cat cag tgc ttc agg ctg gct ctg gtc aac   1344
Gly Asp Thr Asn Leu Ala His Gln Cys Phe Arg Leu Ala Leu Val Asn
        435                 440                 445

aac aac aac cac gcc gag gcc tac aac aac ctg gct gtg ctg gag atg   1392
Asn Asn Asn His Ala Glu Ala Tyr Asn Asn Leu Ala Val Leu Glu Met
    450                 455                 460

cgg aag ggc cac gtt gaa cag gca agg gca cta tta caa act gca tca   1440
Arg Lys Gly His Val Glu Gln Ala Arg Ala Leu Leu Gln Thr Ala Ser
465                 470                 475                 480

tca tta gca ccc cat atg tat gaa ccg cat ttt aat ttt gca aca atc   1488
Ser Leu Ala Pro His Met Tyr Glu Pro His Phe Asn Phe Ala Thr Ile
                485                 490                 495

tct gat aag att gga gat ctg cag aga agc tat gtt gct gcg cag aag   1536
Ser Asp Lys Ile Gly Asp Leu Gln Arg Ser Tyr Val Ala Ala Gln Lys
            500                 505                 510

tct gaa gca gca ttt cca gac cat gtg gac aca caa cat tta att aaa   1584
Ser Glu Ala Ala Phe Pro Asp His Val Asp Thr Gln His Leu Ile Lys
        515                 520                 525

caa tta agg cag cat ttt gct atg ctc tgattgttcc ttagaccaca        1631
Gln Leu Arg Gln His Phe Ala Met Leu
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530 535

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35 40 45
Arg Arg Lys Phe Gln Leu Cys Ala Asp Leu Cys Thr Gln Met Leu Glu
50 55 60
Lys Ser Pro Tyr Asp Gln Ala Ala Trp Ile Leu Lys Ala Arg Ala Leu
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Thr Glu Met Val Tyr Ile Asp Glu Ile Asp Val Asp Gln Glu Gly Ile
85 90 95
Ala Glu Met Met Leu Asp Glu Asn Ala Ile Ala Gln Val Pro Arg Pro
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Gly Thr Ser Leu Lys Leu Pro Gly Thr Asn Gln Thr Gly Gly Pro Ser
115 120 125
Gln Ala Val Arg Pro Ile Thr Gln Ala Gly Arg Pro Ile Thr Gly Phe
130 135 140
Leu Arg Pro Ser Thr Gln Ser Gly Arg Pro Gly Thr Met Glu Gln Ala
145 150 155 160
Ile Arg Thr Pro Arg Thr Ala Tyr Thr Ala Arg Pro Ile Thr Ser Ser
165 170 175
Ser Gly Arg Phe Val Arg Leu Gly Thr Ala Ser Met Leu Thr Ser Pro
180 185 190
Asp Gly Pro Phe Ile Asn Leu Ser Arg Leu Asn Leu Thr Lys Tyr Ser
195 200 205
Gln Lys Pro Lys Leu Ala Lys Ala Cys Leu Ser Ile Ser Phe Ile Met
210 215 220
Lys Met Met Leu Arg Leu Leu Trp Ile Trp Leu Ala Leu Ser Thr Glu

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            260                 265                 270
Ala Leu Lys Gln Gln Glu Met Val Asp Thr Phe Leu Tyr Leu Ala Lys
        275                 280                 285
Val Tyr Val Ser Leu Asp Gln Pro Val Thr Ala Leu Asn Leu Phe Lys
    290                 295                 300
Gln Gly Leu Asp Lys Phe Pro Gly Glu Val Thr Leu Leu Cys Gly Ile
305                 310                 315                 320
Ala Arg Ile Tyr Glu Glu Met Asn Asn Met Ser Ser Ala Ala Glu Tyr
                325                 330                 335
Tyr Lys Glu Val Leu Lys Gln Asp Asn Thr His Val Xaa Ala Ile Ala
            340                 345                 350
Cys Ile Gly Ser Asn His Phe Tyr Ser Asp Gln Pro Glu Ile Ala Leu
        355                 360                 365
Arg Phe Tyr Arg Arg Leu Leu Gln Met Gly Ile Tyr Asn Gly Gln Leu
    370                 375                 380
Phe Asn Asn Leu Gly Leu Cys Cys Phe Tyr Ala Gln Gln Tyr Asp Met
385                 390                 395                 400
Thr Leu Thr Ser Phe Glu Arg Ala Leu Ser Leu Ala Glu Asn Glu Glu
                405                 410                 415
Glu Ala Ala Asp Val Trp Tyr Asn Leu Gly His Val Ala Val Gly Ile
            420                 425                 430
Gly Asp Thr Asn Leu Ala His Gln Cys Phe Arg Leu Ala Leu Val Asn
        435                 440                 445
Asn Asn Asn His Ala Glu Ala Tyr Asn Asn Leu Ala Val Leu Glu Met
    450                 455                 460
Arg Lys Gly His Val Glu Gln Ala Arg Ala Leu Leu Gln Thr Ala Ser
465                 470                 475                 480
Ser Leu Ala Pro His Met Tyr Glu Pro His Phe Asn Phe Ala Thr Ile
                485                 490                 495
Ser Asp Lys Ile Gly Asp Leu Gln Arg Ser Tyr Val Ala Ala Gln Lys
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Ser Glu Ala Ala Phe Pro Asp His Val Asp Thr Gln His Leu Ile Lys
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Gln Leu Arg Gln His Phe Ala Met Leu
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<210> 6
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Ile Gly Val Glu Asn Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly
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tac ctc aca gtg tgc caa gtt act cga gtc tat atc ttt gac tat gga   96
Tyr Leu Thr Val Cys Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly
            20                  25                  30

caa tat tct gct gat ttt tca ggc cca atg atg atc att act cag aag   144
Gln Tyr Ser Ala Asp Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys
        35                  40                  45

atc act agt ttg gct tgc gaa ata cat gat ggg atg ttt cgg aag gat   192
Ile Thr Ser Leu Ala Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp
    50                  55                  60

gaa gaa ctg act tcc tca cag agg gat tta gct gta agg cgc atg cca   240
Glu Glu Leu Thr Ser Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro
65                  70                  75                  80

agc tta ctg gag tat ttg agt tac aac tgt aac ttc atg ggg atc ctg   288
Ser Leu Leu Glu Tyr Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu
                85                  90                  95

gca ggc cca ctt tgc tct tac aaa gac tac att act ttc att gaa ggc   336
Ala Gly Pro Leu Cys Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly
            100                 105                 110

aga tca tac cat atc aca caa tct ggt gaa aat gga aaa gaa gag aca   384
Arg Ser Tyr His Ile Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr
        115                 120                 125

cag tat gaa aga aca gag cca tct cca aat gta agg tca tgagatttat    433
Gln Tyr Glu Arg Thr Glu Pro Ser Pro Asn Val Arg Ser
    130                 135                 140

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cattttcaag ctacagcttc gtggccaaca aagattatct atctgtatat ctctcttttg 613
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<213> Homo sapiens

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Tyr Leu Thr Val Cys Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly
            20   25   30
Gln Tyr Ser Ala Asp Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys
        35   40   45
Ile Thr Ser Leu Ala Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp
    50   55   60
Glu Glu Leu Thr Ser Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro
65   70   75   80
Ser Leu Leu Glu Tyr Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu
                85   90   95
Ala Gly Pro Leu Cys Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly
            100   105   110
Arg Ser Tyr His Ile Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr
        115   120   125
Gln Tyr Glu Arg Thr Glu Pro Ser Pro Asn Val Arg Ser
    130   135   140

<210> 8
<211> 1276
<212> DNA
<213> Homo sapiens

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Ile Gly Val Glu Asn Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly
 1   5   10   15

tac ctc aca gtg tgc caa gtt act cga gtc tat atc ttt gac tat gga 96
Tyr Leu Thr Val Cys Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly
            20   25   30

caa tat tct gct gat ttt tca ggc cca atg atg atc att act cag aag 144
Gln Tyr Ser Ala Asp Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys
        35   40   45

atc act agt ttg gct tgc gaa ata cat gat ggg atg ttt cgg aag gat 192
Ile Thr Ser Leu Ala Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp
    50   55   60

gaa gaa ctg act tcc tca cag agg gat tta gct gta agg cgc atg cca 240

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Glu Glu Leu Thr Ser Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro
 65                  70                  75                  80

agc tta ctg gag tat ttg agt tac aac tgt aac ttc atg ggg atc ctg   288
Ser Leu Leu Glu Tyr Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu
                 85                  90                  95

gca ggc cca ctt tgc tct tac aaa gac tac att act ttc att gaa ggc   336
Ala Gly Pro Leu Cys Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly
            100                 105                 110

aga tca tac cat atc aca caa tct ggt gaa aat gga aaa gaa gag aca   384
Arg Ser Tyr His Ile Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr
        115                 120                 125

cag tat gaa aga aca gna gcc atc tcc aaa tgt aag gtc atg aga ttt   432
Gln Tyr Glu Arg Thr Xaa Ala Ile Ser Lys Cys Lys Val Met Arg Phe
    130                 135                 140

atc tgg agc ctt tac agc atg tat tgn act gcg gkt gtt cag aag ctc   480
Ile Trp Ser Leu Tyr Ser Met Tyr Xaa Thr Ala Xaa Val Gln Lys Leu
145                 150                 155                 160

tta gtt tgt ggg ctg tcc ttg tta ttt cac ttg acc atc tgt aca aca   528
Leu Val Cys Gly Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr
                165                 170                 175

tta cct gtg gag tac aac att gat gag cat ttt caa gct aca gct tcg   576
Leu Pro Val Glu Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser
            180                 185                 190

tgg cca aca aag att atc tat ctg tat atc tct ctt ttg gct gcc aga   624
Trp Pro Thr Lys Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg
        195                 200                 205

ccc aaa tac tat ttt gca tgg acg cta gct gat gcc att aat aat gct   672
Pro Lys Tyr Tyr Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala
    210                 215                 220

gca ggc ttt ggt ttc aga ggg tat gac gaa aat gga gca gct cgc tgg   720
Ala Gly Phe Gly Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp
225                 230                 235                 240

gac tta att tcc aat ttg aga att caa caa ata gag atg tca aca agt   768
Asp Leu Ile Ser Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser
                245                 250                 255

ttc aag atg ttt ctt gat aat tgg aat att cag aca gct ctt tgg ccc   816
Phe Lys Met Phe Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Pro
            260                 265                 270

aaa agg gtg tgt tat gaa cga acc tcc ttc agt cca act atc cag acg   864
Lys Arg Val Cys Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr
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        275                 280                 285

ttc att ctc cct gcc att ntg gca cgg ggt ata ccc agg ata tta tct   912
Phe Ile Leu Pro Ala Ile Xaa Ala Arg Gly Ile Pro Arg Ile Leu Ser
    290                 295                 300

aac gtt tct aac agg ggt gtt aat gac att agc agc aga gct atg aga   960
Asn Val Ser Asn Arg Gly Val Asn Asp Ile Ser Ser Arg Ala Met Arg
305                 310                 315                 320

aat aac ttt aga cat tat ttc att gaa cct tcc caa ctg aaa tta ttt   1008
Asn Asn Phe Arg His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe
                325                 330                 335

tat gat gtt mta aca tgg ata gta aac tca agt agc aat aag tta cac   1056
Tyr Asp Val Xaa Thr Trp Ile Val Asn Ser Ser Ser Asn Lys Leu His
            340                 345                 350

agk tgk gsc att tgt gct tct ttc tat waa acc atc act cac rkt tya   1104
Xaa Xaa Xaa Ile Cys Ala Ser Phe Tyr Xaa Thr Ile Thr His Xaa Xaa
        355                 360                 365

cag gtc cgg ttt att gcc gga cat act ggt tcc tcg ata atg gcg tgc   1152
Gln Val Arg Phe Ile Ala Gly His Thr Gly Ser Ser Ile Met Ala Cys
    370                 375                 380

cgg aca acg cgg aga aag gta ctg gaa gtt ccg ctc cac caa gtc gtg   1200
Arg Thr Thr Arg Arg Lys Val Leu Glu Val Pro Leu His Gln Val Val
385                 390                 395                 400

ggg gac act tgg gac agc tct tcc aca agc gcg ccg aag ccg gac aca   1248
Gly Asp Thr Trp Asp Ser Ser Ser Thr Ser Ala Pro Lys Pro Asp Thr
                405                 410                 415

acg acg ggg cgg ggg ggt ggg gca acc c                            1276
Thr Thr Gly Arg Gly Gly Gly Ala Thr
            420                 425
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<210> 9
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
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<223> Xaa = Any Amino Acid

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Ile Gly Val Glu Asn Met His Asn Tyr Cys Phe Val Phe Ala Leu Gly
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Tyr Leu Thr Val Cys Gln Val Thr Arg Val Tyr Ile Phe Asp Tyr Gly
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            20                  25                  30
Gln Tyr Ser Ala Asp Phe Ser Gly Pro Met Met Ile Ile Thr Gln Lys
        35                  40                  45
Ile Thr Ser Leu Ala Cys Glu Ile His Asp Gly Met Phe Arg Lys Asp
    50                  55                  60
Glu Glu Leu Thr Ser Ser Gln Arg Asp Leu Ala Val Arg Arg Met Pro
65                  70                  75                  80
Ser Leu Leu Glu Tyr Leu Ser Tyr Asn Cys Asn Phe Met Gly Ile Leu
                85                  90                  95
Ala Gly Pro Leu Cys Ser Tyr Lys Asp Tyr Ile Thr Phe Ile Glu Gly
            100                 105                 110
Arg Ser Tyr His Ile Thr Gln Ser Gly Glu Asn Gly Lys Glu Glu Thr
        115                 120                 125
Gln Tyr Glu Arg Thr Xaa Ala Ile Ser Lys Cys Lys Val Met Arg Phe
    130                 135                 140
Ile Trp Ser Leu Tyr Ser Met Tyr Xaa Thr Ala Xaa Val Gln Lys Leu
145                 150                 155                 160
Leu Val Cys Gly Leu Ser Leu Leu Phe His Leu Thr Ile Cys Thr Thr
                165                 170                 175
Leu Pro Val Glu Tyr Asn Ile Asp Glu His Phe Gln Ala Thr Ala Ser
            180                 185                 190
Trp Pro Thr Lys Ile Ile Tyr Leu Tyr Ile Ser Leu Leu Ala Ala Arg
        195                 200                 205
Pro Lys Tyr Tyr Phe Ala Trp Thr Leu Ala Asp Ala Ile Asn Asn Ala
    210                 215                 220
Ala Gly Phe Gly Phe Arg Gly Tyr Asp Glu Asn Gly Ala Ala Arg Trp
225                 230                 235                 240
Asp Leu Ile Ser Asn Leu Arg Ile Gln Gln Ile Glu Met Ser Thr Ser
                245                 250                 255
Phe Lys Met Phe Leu Asp Asn Trp Asn Ile Gln Thr Ala Leu Trp Pro
            260                 265                 270
Lys Arg Val Cys Tyr Glu Arg Thr Ser Phe Ser Pro Thr Ile Gln Thr
        275                 280                 285
Phe Ile Leu Pro Ala Ile Xaa Ala Arg Gly Ile Pro Arg Ile Leu Ser
    290                 295                 300
Asn Val Ser Asn Arg Gly Val Asn Asp Ile Ser Ser Arg Ala Met Arg
305                 310                 315                 320
Asn Asn Phe Arg His Tyr Phe Ile Glu Pro Ser Gln Leu Lys Leu Phe
                325                 330                 335
Tyr Asp Val Xaa Thr Trp Ile Val Asn Ser Ser Ser Asn Lys Leu His
            340                 345                 350
Xaa Xaa Xaa Ile Cys Ala Ser Phe Tyr Xaa Thr Ile Thr His Xaa Xaa
        355                 360                 365
Gln Val Arg Phe Ile Ala Gly His Thr Gly Ser Ser Ile Met Ala Cys
    370                 375                 380
Arg Thr Thr Arg Arg Lys Val Leu Glu Val Pro Leu His Gln Val Val
385                 390                 395                 400
Gly Asp Thr Trp Asp Ser Ser Ser Thr Ser Ala Pro Lys Pro Asp Thr
                405                 410                 415
Thr Thr Gly Arg Gly Gly Gly Ala Thr
            420                 425
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<210> 10
<211> 29
<212> DNA
<213> Homo sapiens

<400> 10
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<210> 11
<211> 28
<212> DNA
<213> Homo sapiens

<400> 11
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